



SEQUENCE LISTING

<110> MA, Jing
GUO, Yajun

<120> PREPARATION AND APPLICATION OF
ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

<130> 047630-0301

<140> US 10/723,003
<141> 2003-11-26

<150> CN 2003101199300
<151> 2003-11-25

<150> CN 031292909
<151> 2003-06-13

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 546
<212> DNA
<213> Homo sapiens

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120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgccttcc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagca gctggtgccg
420
ctgaaggccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactccctcaa ccctgccacc cccatggagt cccccggccccc tggaggccac agccccgaca
540
gccccg
546

<210> 2
<211> 182
<212> PRT
<213> Homo sapiens

<400> 2

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu
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Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe
															20
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
															35
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
															50
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
															65
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
															85
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
															100
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
															115
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
															130
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
															145
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
															165
Thr	Ala	Pro	Thr	Ala	Pro										180

<210> 3
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
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agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggccgctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcacaaa tgtgccttgc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagca gctggtgccg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccgcccccc tggaggccac agccccgaca
540
gccccggagc ccaaattttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctttc ccccaaaac ccaaggacac cctcatgatc
660

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggc
720
aagttaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtcaaggc tcacaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca
960
tcccggatg agctgaccaa gaaccaggc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtggagagc aatggcagc cgagaaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tcatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctccggta aa
1242

<210> 4
<211> 414
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160
Asp Ser Ser Thr Leu Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180 185 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195 200 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

210	215	220													
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
225							230				235				240
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
							245				250				255
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
							260				265				270
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
							275				280				285
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
							290				295				300
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
305							310				315				320
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
							325				330				335
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
							340				345				350
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
							355				360				365
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
							370				375				380
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
385							390				395				400
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
					405						410				

<210> 5
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 5
 ggcgggtggag gctctggtgg aggcggttca ggaggcggtg gatct
 45

<210> 6
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10 15

<210> 7
 <211> 426
 <212> DNA
 <213> Mus musculus

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<400> 7
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60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca
120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc
240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc
300
acagcctaca tggagcttag cagactgacc tctgaggact ctgcggctta ttattgtgtc
360
tacggtagta ggtacgactg gtattnatgt gtctgggcg cagggaccac ggtcacccgtc
420
tcctca
426

<210> 8
<211> 138
<212> PRT
<213> Mus musculus

<400> 8
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
115 120 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135

<210> 9
<211> 465
<212> DNA
<213> Mus musculus

<400> 9
atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc
60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctggtacc
120
tgtggaaaca ttatgtatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag
180

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gtcactatga gctgtaagtc cagtcaaagt gtttatataca gttcaaataca gaagaactac
240
ttggcctggc accagcagaa accaggcag ttcctaaac tgctgatcta ctggcatcc
300
actaggaaat ctgggtccc tgatcgctc acaggcagtg gatctggac agatttact
360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc
420
tcctcataca cgttcgagg ggggaccaag ctggaaataa agcgg
465

<210> 10
<211> 133
<212> PRT
<213> Mus musculus

<400> 10
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
20 25 30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Thr Lys
115 120 125
Leu Glu Ile Lys Arg
130

<210> 11
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
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120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
180
aaggcagaagc ctgggcaggc ctttgactgg attggatata ttgttcctta caatgatggc
240
actaagtaca atgagaagtt caaaggcaag gccacactga ctccagacaa atcctccagc
300

acagcctaca tggagcttag cagactgacc tctgaggact ctgcggtcta ttattgtgc
360
tacggtagta ggtacgactg gtathtagat gtctgggcg cagggaccac ggtcaccgtc
420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
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600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggg cagcacaggg agggagggtg tctgctggaa gcaggcttag cgctcctgcc
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840
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900
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960
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1020
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1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctgcctcc agctcaaggc gggacaggtg
1200
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1320
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1380
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1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtggacc cgtgggtgc
1620
gagggccaca tggacagagg ccggctcggtc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccggaa gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcagggggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980

actacacgca gaagagcctc tccctgtctc ccggtaaatg a
2021

<210> 12
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
115 120 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225 230 235 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
290 295 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305 310 315 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
340 345 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

355	360	365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val		
370	375	380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val		
385	390	395
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
405	410	415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr		
420	425	430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
435	440	445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
450	455	460
Ser Pro Gly Lys		
465		

<210> 13

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 13

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120
tgtggaaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaaag
180
gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaataca gaagaactac
240
ttggcctggc accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc
300
actaggaaat ctgggtgtccc tgatcgcttc acaggcagtg gatctggac agattttact
360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc
420
tcctcataca cgttcgagg ggggaccaag ctggaaataa agcggactgt ggctgcacca
480
tctgtcttca tcttcccccc atctgatgag cagttgaaat ctggaaactgc ctctgttgc
540
tgccctgctga ataacttcta tcccagagag gccaaagtac agtggaaaggt ggataacgcc
600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac
660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc
720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa cagggagag
780
tgttag
786

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<210> 14

<211> 239

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
20 25 30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Thr Lys
115 120 125
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 15
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt
60
gtccactccc aggtgcagct ggtgcagtct ggccggtgag tggccagcc cggccgcagc
120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtat gacatgggt
180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt
240

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actaagtaca atgaaaagg ttacaatata caagtacaa gagcaagtca
300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccggcgata ctattgtgtg
360
cgcggcagcc gttacgactg gtacttggac tactgggccc aaggcactcc agtcaccgtc
420
tcctct
426

<210> 16
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1 . 5 10 15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
20 25 30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
85 90 95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
115 120 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser
130 135

<210> 17
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
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atggattttc aagtgcagat tttcagcttc ctgctaata cgtgttcagt cataatgtcc
120
agagggaaaca tcatgatgac tcagagccca tccagcttga gcgcattcgtt aggcgaccgc
180
gtaacgatca cttgcaaatac ctctcagtcgtt gtattgtact ccagcaacca gaagaactac
240
ctggccggat atcagcagac tccccggcaaa gccccaaagt tgctgattta ttgggcctcc
300

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acgcgcgagt ctggcgtgcc atcacgctt agcggcagcg ggtccggta c agattacacg
360
tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtagttt
420
agttccataca cttttggcca ggaaactaaa ctgcagatta ctcga
465

<210> 18
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
35 40 45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Ile Tyr Trp Ala Ser
65 70 75 80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
85 90 95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
100 105 110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
115 120 125
Thr Lys Leu Gln Ile Thr Arg
130 135

<210> 19
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
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gtccactccc aggtgcagct ggtgcagtct ggcgggtggag tggccagcc cggccgcagc
120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggt
180
cgccaaagccc cccgaaaggc cctcgaatgg attggctaca ttgtgcctta taatgacgg
240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca
300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccggcgtata ctattgtgt
360

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cgcggcagcc gttacgactg gtacttggac tactgggcc aaggcactcc agtcaccgtc
420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttggaa actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
660
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720
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780
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840
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960
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1020
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1080
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1140
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1200
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1260
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1320
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1380
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1440
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1560
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1620
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1680
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1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagttgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccggtct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcagggaaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a
2021

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<210> 20
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1           5           10          15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
 20          25          30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35          40          45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50          55          60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65          70          75          80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
 85          90          95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
100         105         110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
115         120         125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130         135         140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145         150         155         160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165         170         175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180         185         190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195         200         205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210         215         220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225         230         235         240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245         250         255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260         265         270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275         280         285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
290         295         300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305         310         315         320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325         330         335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
340         345         350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355         360         365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
370         375         380

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Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys
 465

<210> 21
 <211> 786
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 21
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 atggattttc aagtgcagat tttcagcttc ctgctaataca gtgttcaactt cataatgtcc
 120
 agagggaaaca tcatgtatgac tcagagccca tccagcttga ggcgcataactt agggcgaccgc
 180
 gtaacgatca cttgcaaatac ctctcagtcgtca gtattgtact ccagcaacca gaagaactac
 240
 ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc
 300
 acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtaac agattacacg
 360
 tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt
 420
 agttcctaca cttttggcca gggaaactaaa ctgcagatcca ctcgaactgt ggctgcacca
 480
 tctgtttca tcttcccgcc atctgatgag cagttgaaat ctggaaactgc ctctgttg
 540
 tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaagggt ggataacgcc
 600
 ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac
 660
 agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc
 720
 tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag
 780
 tgttag
 786

 <210> 22
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 22

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
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Val	Ile	Met	Ser	Arg	Gly	Asn	Ile	Met	Met	Thr	Gln	Ser	Pro	Ser	Ser
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ser	Ser
35															
Gln	Ser	Val	Leu	Tyr	Ser	Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr
50															
55															
Gln	Gln	Thr	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Ile	Tyr	Trp	Ala	Ser	
65															
70															
Thr	Arg	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly		
85															
90															
Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala
100															
105															
Thr	Tyr	Tyr	Cys	His	Gln	Tyr	Phe	Ser	Ser	Tyr	Thr	Phe	Gly	Gln	Gly
115															
120															
Thr	Lys	Leu	Gln	Ile	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile
130															
135															
140															
Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val
145															
150															
155															
160															
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys
165															
170															
175															
Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu
180															
185															
190															
Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu
195															
200															
205															
Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr
210															
215															
220															
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu
225															
230															
235															
240															
300															

<210> 23

<211> 2489

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 23

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ctgaggctgt cctgcaaggc atctggctac acttcacca gctacgtat gacatgggt 180
cgccaaagccc ccggaaaggc cctcgaatgg attggctaca ttgtgcctta taatgacgg 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300

accgcattcc tccaaatgga cagcttcgtt ccagaggaca ccggcgata ctattgttg
360
cgcggcagcc gttacgactg gtacttggac tactgggccc aaggcactcc agtcaccgtc
420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
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660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
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1140
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1800
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1920
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1980

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 2040
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 2400
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 2460
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 2489

<210> 24
 <211> 624
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

Met	Asp	Trp	Val	Trp	Thr	Leu	Leu	Phe	Leu	Leu	Ser	Val	Thr	Ala	Gly
1					5				10				15		
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln
					20				25				30		
Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
					35			40				45			
Thr	Ser	Tyr	Val	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					50			55				60			
Glu	Trp	Ile	Gly	Tyr	Ile	Val	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn
					65			70			75			80	
Glu	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ser	Asp	Lys	Ser	Lys	Ser
					85			90				95			
Thr	Ala	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val
					100			105				110			
Tyr	Tyr	Cys	Ala	Arg	Gly	Ser	Arg	Tyr	Asp	Trp	Tyr	Leu	Asp	Tyr	Trp
					115			120				125			
Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
					130			135				140			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
					145			150			155			160	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
					165			170				175			
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
					180			185				190			
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
					195			200				205			
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
					210			215				220			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Val	Glu	Pro	Lys	Ser	

225	230	235	240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys	Pro Ala Pro Glu Leu Leu		
245	250	255	
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu			
260	265	270	
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser			
275	280	285	
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu			
290	295	300	
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr			
305	310	315	320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
325	330	335	
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
340	345	350	
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
355	360	365	
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
370	375	380	
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
385	390	395	400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
405	410	415	
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
420	425	430	
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
435	440	445	
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
450	455	460	
Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser			
465	470	475	480
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln			
485	490	495	
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys			
500	505	510	
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu			
515	520	525	
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn			
530	535	540	
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser			
545	550	555	560
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr			
565	570	575	
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe			
580	585	590	
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro			
595	600	605	
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro			
610	615	620	

<210> 25
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 25
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120
ctgaggctgt cctgcaaggc atctggctac acttcacca gctacgtat gacatgggt
180
cgccaagccc ccggaaaggg cctcaaatgg attggctaca ttgtgcctta taatgacgg
240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca
300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgcccgtata ctattgtgt
360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc
420
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480
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660
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1140
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1200
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1380
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1620

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 1680
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 2340
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<210> 26
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26
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 Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
 85 90 95
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 465 470 475 480
 Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
 485 490 495
 Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
 500 505 510
 Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
 515 520 525
 Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
 530 535 540
 Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
 545 550 555 560
 Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys

565	570	575
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser		
580	585	590
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser		
595	600	605
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro		
610	615	620
Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro		
625	630	635

<210> 27
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27
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240
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300
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420
ctgaaggccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
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660
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780
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1080

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
 1140
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 1200
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 1260
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 1380
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 1440
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 1500
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 1800
 ctgatttatt gggcctccac ggcgagatct ggcgtgccat cacgctttag cggcagcggg
 1860
 tccggtag attacacgtt taccattagc agtctgcagc ctgaggacat agccacctac
 1920
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 1980
 cgatga
 1986

<210> 28

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu
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Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	
															20
															25
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
															30
															35
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
															40
															45
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Gln	
															50
															55
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
															60
															65
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
															70
															75
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
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															85
															90
															95
															100
															105
															110

	115	120	125												
Arg	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	
130					135					140					
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
145					150				155				160		
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
				165					170				175		
Thr	Ala	Pro	Thr	Ala	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
				180				185				190			
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
				195				200				205			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
				210			215			220					
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
225				230				235				240			
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
				245				250				255			
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
				260				265				270			
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
				275				280				285			
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
				290				295				300			
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
305				310					315				320		
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
				325					330				335		
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
				340				345				350			
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
				355				360				365			
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
				370				375				380			
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
385				390					395				400		
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Gln	Val
				405					410				415		
Gln	Leu	Val	Gln	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	
				420				425				430			
Arg	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Val	Met
				435				440				445			
His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr
				450				455				460			
Ile	Val	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn	Glu	Lys	Phe	Lys	Gly
465				470					475				480		
Arg	Phe	Thr	Ile	Ser	Ser	Asp	Lys	Ser	Lys	Ser	Thr	Ala	Phe	Leu	Gln
				485					490				495		
Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
				500					505				510		
Gly	Ser	Arg	Tyr	Asp	Trp	Tyr	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Pro
				515					520				525		
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
				530				535				540			
Gly	Gly	Gly	Ser	Asn	Ile	Met	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser
545				550					555				560		
Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ser	Ser	Gln	Ser
				565					570				575		

Val	Leu	Tyr	Ser	Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln
580							585							590	
Thr	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
595							600							605	
Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
610							615							620	
Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr
625							630							635	
Tyr	Cys	His	Gln	Tyr	Phe	Ser	Ser	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
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645														655	
Leu	Gln	Ile	Thr	Arg											
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<210> 29

<211> 2489

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 29

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2489

<210> 30
<211> 624
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

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Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
115 120 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225 230 235 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
290 295 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305 310 315 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
340 345 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
370 375 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
420 425 430

Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
435						440						445			
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
450						455					460				
Ser	Pro	Gly	Lys	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
465						470				475					480
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
						485			490					495	
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys
									505					510	
Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu
								515	520			525			
Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn
							530	535			540				
Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser
545						550				555					560
Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr
								565	570			575			
Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe
							580	585			590				
Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Pro
							595	600			605				
Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr	Ala	Pro
							610	615			620				

<210> 31
 <211> 2534
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 31
 cttgccgcca ccatggaaatg gagttggata tttctcttgc tcctgtcagg aactgcagg
 60
 gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca
 120
 gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
 180
 aagcagaagc ctgggcaggc ctttgactgg attggatata ttgttcctta caatgatggc
 240
 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc
 300
 acagcttaca tggagcttag cagactgacc tctgaggact ctgcggctta ttatttgtgc
 360
 tacggtagta ggtacgactg gtattnagat gtctggggcg cagggaccac ggtcaccggtc
 420
 tcctcagcta gcaccaaggc cccatcggtc ttccccctgg caccctcctc caagagcacc
 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
 540
 gtgtcttggc actcaggcgc cctgaccaggc ggcgtgcaca ctttcccggc tgtcctacag
 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
 660

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcg cgctcctgcc
780
tggacgcata ccggctatgc agccccagtc cagggcagca aggaggccc cgtctgcctc
840
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900
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960
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1020
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1080
tccagtaact cccaatcttc tctctgcaga gcccaaattct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggttaagc cagcccaggc ctgcctcc agctcaaggc gggacaggtg
1200
cccttagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacccca
1260
tctcttcctc agcacctgaa ctccctgggg gaccgtcagt cttcctcttc ccccaaaaac
1320
ccaaggacac cctcatgatc tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgt a cccgggtggc tgcgtcctca
1500
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1560
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1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctccctgtct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtgaggc tctggtgag
2040
gcgggttcagg aggccgtgga tctacccagg actgctcctt ccaacacagc cccatctct
2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca
2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggcctgg
2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg
2280
agcgcgtgaa cacggagata cactttgtca ccaaattgtgc ctttcagccc ccccccagct
2340

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gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg
2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc
2460
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2520
cgacagcccc gtga
2534

<210> 32
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
115 120 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225 230 235 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
290 295 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

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305	310	315	320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
325	330	335	
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
340	345	350	
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
355	360	365	
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
370	375	380	
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
385	390	395	400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
405	410	415	
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
420	425	430	
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
435	440	445	
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
450	455	460	
Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly			
465	470	475	480
Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser			
485	490	495	
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp			
500	505	510	
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly			
515	520	525	
Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys			
530	535	540	
Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr			
545	550	555	560
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys			
565	570	575	
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser			
580	585	590	
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser			
595	600	605	
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro			
610	615	620	
Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro			
625	630	635	

<210> 33
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
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agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120

tgcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggccgctggc cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggcgtt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgccctc ctgcaggaga cctccgagca gctggtgcc
420
ctgaagccct ggatcaactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccgcccccc tggaggccac agccccgaca
540
gccccggagc ccaaatttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctgggg gaccgtcagt cttcctttc ccccaaaaac ccaaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcggag
780
gagcagtaca acagcacgta ccgggtggc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtcaaggc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca
960
tcccggatg agctgaccaa gaaccaggc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgcccgtgga gtggagagc aatgggcagc cggagaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg ttagtgcataa ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctccggta aagaggtcca gctgcagcag
1260
tctggacctg agctggtaaa gcctgggct tcagtgaaga tgcctgcaa ggcttctgga
1320
tacacattca ctagctatgt tatgcactgg gtgaagcaga agcctggca gggccttgac
1380
tggattggat atattgttcc ttacaatgtat ggcactaagt acaatgagaa gttcaaaggc
1440
aaggccacac tgacttcaga caaatcctcc agcacagcct acatggagct cagcagactg
1500
acctctgagg actctgcggc ctattattgt gtctacggta gttagtgcataa ctggattta
1560
gatgtctggc ggcagggac cacggtcacc gtctcctcag gcggtggagg ctctgggta
1620
ggcggttcag gaggcgggtgg atctaaccatt atgatgacac agtcgccatc atctctggct
1680
gtgtctgcag gagaaaaggt cactatgagc tgtaagtcca gtcaaagtgt tttatacagt
1740
tcaaattcaga agaactactt ggcctggta cagcagaaac cagggcagtc tcctaaactg
1800

ctgatctact gggcatccac taggaaatct ggtgtccctg atcgcttcac aggcagtgga
 1860
 tctggacag attttactct taccatcagc agtgtacaag ctgaagacct ggcagtttat
 1920
 tactgtcatac aatatattctc ctcatacacg ttcggagggg ggaccaagct ggaaataaaag
 1980
 cggtga
 1986

<210> 34
 <211> 661
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 34

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu
1							5		10				15		
Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe
							20		25				30		
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
							35		40			45			
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
							50		55			60			
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
65							70			75			80		
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
							85			90			95		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
							100		105			110			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
							115		120			125			
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
							130		135			140			
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
145							150			155			160		
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
							165			170			175		
Thr	Ala	Pro	Thr	Ala	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
							180		185			190			
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
							195		200			205			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
							210		215			220			
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
225							230			235			240		
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
							245			250			255		
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
							260		265			270			
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
							275		280			285			
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
							290		295			300			

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 305 310 315 320
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 325 330 335
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 340 345 350
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 355 360 365
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 370 375 380
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 385 390 395 400
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val
 405 410 415
 Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
 420 425 430
 Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
 435 440 445
 His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Asp Trp Ile Gly Tyr
 450 455 460
 Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
 465 470 475 480
 Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
 485 490 495
 Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Tyr
 500 505 510
 Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr
 515 520 525
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 530 535 540
 Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
 545 550 555 560
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
 565 570 575
 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 580 585 590
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 595 600 605
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 610 615 620
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
 625 630 635 640
 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
 645 650 655
 Leu Glu Ile Lys Arg
 660

<210> 35
 <211> 426
 <212> DNA
 <213> Mus musculus

<400> 35
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 60

tcccaggtac aactacagca gcctgggct gagctggta agcctgggc ctcagtgaag
120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag
180
acacctggtc ggggcctgga atggattgga gctatttac caggaaatgg tgataacttcc
240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc
300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg
360
acttactacg gcggtgactg gtacttcaat gtctgggcn cagggaccac ggtcaccgtc
420
tctgca
426

<210> 36
<211> 140
<212> PRT
<213> Mus musculus

<400> 36
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1 5 10 15
Val His Ser Gln Val Gln Leu Gln Pro Gly Ala Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
50 55 60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65 70 75 80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
115 120 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
130 135 140

<210> 37
<211> 390
<212> DNA
<213> Mus musculus

<400> 37
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tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgcatt tccagggag
120
aaggtcacaa tgacttgcag ggccagctca agtgtaagtt acatccactg gttccagcag
180
aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc
240
cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg
300

gaggctgaag atgctgccac ttattactgc cagcagtggc ctagtaaccc acccacgttc
 360
 ggtggtggc ccaagctggc gatcaaacgc
 390

<210> 38
 <211> 129
 <212> PRT
 <213> Mus musculus

<400> 38
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125
 Arg

<210> 39
 <211> 2021
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 39
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 60
 tcccaggtac aactacagca gcctggggct gagctggta agcctggggc ctcagtgaaag
 120
 atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag
 180
 acacctggtc ggggcctgga atggattgga gctatttatac cagggaaatgg tgataacttcc
 240
 tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc
 300
 tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg
 360
 acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc
 420
 tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
 480

tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
 540
 gtgtcttggaa actcaggcgcc cctgaccagc ggcgtgcaca cttcccgcc tgtcctacag
 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
 720
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 780
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 840
 ttcacccgga gcctctgccc gccccactca tgctcaggaa gagggtcttc tggcttttc
 900
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 960
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 1020
 cccacccaa aggccaaact ctccactccc ttagctcgaa caccttctct cctccagat
 1080
 tccagtaact cccaatcttc tctctgcaga gcccaaattct tgtgacaaaaa ctcacacatg
 1140
 cccaccgtgc ccaggtaagc cagcccaggg ctcgcccctcc agctcaaggc gggacaggtg
 1200
 cccttagagta gcctgcattcc agggacaggg cccagccggg tgctgacacg tccacacctca
 1260
 tctcttcctc agcacctgaa ctccctgggg gaccgtcagt cttcctcttc ccccaaaaac
 1320
 ccaaggacac cctcatgatc tcccgacccc ctgaggtcac atgcgtggtg gtggacgtga
 1380
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
 1440
 ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
 1500
 ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtcaaggc tccaacaaag
 1560
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtgc
 1620
 gagggccaca tggacagagg ccggctcgcc ccaccctctg ccctgagagt gaccgctgta
 1680
 ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc
 1740
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
 1800
 gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
 1860
 ctcggctgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
 1920
 gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
 1980
 actacacgca gaagagcctc tccctgtctc ccggtaaatg a
 2021

<210> 40
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1 5 10 15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
50 55 60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65 70 75 80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Gly Gly Asp Trp Tyr Phe Asn
115 120 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
130 135 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225 230 235 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255
Leu Leu Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
290 295 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
370 375 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460
Ser Leu Ser Pro Gly Lys
465 470

<210> 41
<211> 711

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
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tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgc atc tccaggggag
120
aaggcacaa tgacttgca g gccagctca agt gtaagtt acatccactg gttccagc ag
180
aagccaggat cctccccaa accctggatt tatgccacat ccaacctggc ttctggagtc
240
cctgttcgct tcagtgccag tgggtctggg acctcttact ctctcacaat cagtagagtg
300
gaggctgaag atgctgccac ttattactgc cagcagtgga ctagtaaccc acccacgttc
360

ggtggggaa ccaagctgg a gatcaa acg a actgtggctg caccatctgt cttcatcttc
420
ccgccccatctg atgagcagg t gaaatctgg a actgcctctg ttgtgtgc ct gctgaataac
480
ttctatccca gagaggccaa agtacagtgg aagggtggata acgcctcca atcgggtaac
540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagc ct cagcagcacc
600
ctgacgctga gcaaaggcaga ctacgagaaa cacaagg tct acgcctgc gta agtcacccat
660
cagggcctga gctcgccctg cacaaggc ttcaacagg g gagggtt a g
711

<210> 42
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20						25					30	
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
			35				40					45			
Ser	Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser
			50			55				60					
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	65			70					75					80	
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85				90					95			
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100				105					110			
Thr	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
	115				120				125						
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
	130				135				140						
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
	145			150					155				160		
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
					165			170				175			
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
			180				185				190				
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
	195					200			205						
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
			210				215				220				
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
	225				230				235						

<210> 43
 <211> 2489
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 43
 gccaccatgg gattcagcag gatctttctc ttccctcctgt cagtaactac aggtgtccac
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 tcccaggtagc aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag
 120
 atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag
 180
 acacctggtc ggggcctgga atggatttggaa gctattttatc cagggaaatgg tgataacttcc
 240
 tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaattcctc cagcacagcc
 300
 tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg
 360
 acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc
 420
 tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
 480

tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgg aactcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggg cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcattc ccggctatgc agccccagtc cagggcagca aggccaggccc cgtctgcctc
840
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900
ccaggctctg ggcaggcaca .ggcttaggtgc ccctaaccctt ggcctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccggag gaccctgccc ctgacctaag
1020
cccacccaa aggccaaact ctccactccc tcagctcgga caccttctct cctccagat
1080
tccagtaact ccaatcttc tctctgcaga gcccaaactt tgcataaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggg ctcgcctcc agctcaaggc gggacaggtg
1200
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1260
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1320
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1380
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1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgctcctca
1500
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1620
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1800
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1860
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1920
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2040
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2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct
2160

ggcggctggc cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga
 2220
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 2280
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 2340
 cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc
 2400
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 2460
 tggaggccac agccccgaca gccccgtga
 2489

<210> 44
 <211> 626
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 44

Met	Gly	Phe	Ser	Arg	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Val	Thr	Thr	Gly
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Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys
								20		25				30	
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
								35		40			45		
Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu
								50		55			60		
Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn
								65		70		75		80	
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
								85		90			95		
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
								100		105			110		
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn
								115		120			125		
Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys
								130		135			140		
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly
								145		150			155		160
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
								165		170			175		
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
								180		185			190		
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
								195		200			205		
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn
								210		215			220		
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro
								225		230			235		240
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
								245		250			255		
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
								260		265			270		
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp

275	280	285
Val Ser His Glu Pro Glu Val	Lys Phe Asn Trp Tyr	Val Asp Asp Gly
290	295	300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn		
305	310	315
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp		
325	330	335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro		
340	345	350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu		
355	360	365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn		
370	375	380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
385	390	395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr		
405	410	415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
420	425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
435	440	445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
450	455	460
Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro		
465	470	475
Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu		
485	490	495
Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu		
500	505	510
Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu		
515	520	525
Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg		
530	535	540
Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro		
545	550	555
Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln		
565	570	575
Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln		
580	585	590
Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr		
595	600	605
Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr		
610	615	620
Ala Pro		
625		

<210> 45
 <211> 2534
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 45

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tcccaggtagc aactacagca gcctgggct gagctggta agcctgggc ctcagtgaag
120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg gttaaagcag
180
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240
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300
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360
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420
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480
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540
gtgtcttggaa actcaggcgc cctgaccagc ggcgtgcaca cttcccgcc tgtcctacag
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660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
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780
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840
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900
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960
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1020
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1080
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1140
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1320
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1380
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1680

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 1920
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 1980
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 2160
 ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggcctgg
 2220
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 2280
 agcgcgtgaa cacggagata cacttgtca ccaaattgtgc ctttcagccc ccccccaagct
 2340
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 2400
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 2460
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 2520
 cgacagcccc gtga
 2534

<210> 46
 <211> 641
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 46
 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
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 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60
 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125
 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys

130	135	140
Gly	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly	
145	150	155
Gly	Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro	160
	165	170
Val	Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr	175
	180	185
Phe	Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val	190
	195	200
Val	Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn	205
	210	215
Val	Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro	220
	225	230
Lys	Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu	235
	245	250
Leu	Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	255
	260	265
Thr	Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	270
	275	280
Val	Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly	285
	290	295
Val	Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn	300
	305	310
Ser	Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	315
	325	330
Leu	Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	335
	340	345
Ala	Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	350
	355	360
Pro	Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	365
	370	375
Gln	Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	380
	385	390
Ala	Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	395
	405	410
Thr	Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	400
	420	425
Leu	Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	430
	435	440
Ser	Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	445
	450	455
Ser	Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser	460
	465	470
Gly	Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile	475
	485	490
Ser	Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu	495
	500	505
Gln	Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu	510
	515	520
Cys	Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg	525
	530	535
Leu	Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val	540
	545	550
Asn	Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro	555
	565	570
Ser	Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu	560
	575	

580	585	590
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn		
595	600	605
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu		
610	615	620
Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala		
625	630	635
Pro		640

<210> 47
<211> 1974
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47
atgacagtgc tggcgccagc ctggagccca acaacctatac tcctcctgct gctgctgctg
60
agctcgggac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggc cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcacaaa tgtgccttgc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgccctc ctgcaggaga cctccgagca gctggtgccg
420
ctgaagccct ggatcaactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca
540
gccccggagc ccaaatttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttccttgc ccccaaaaac ccaaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gcccggggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggc tccaaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca
960
tcccggatg agctgaccaa gaaccaggc agcctgaccc gcctggtcaa aggcttctat
1020
cccagcgaca tcgcccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080

acgcctcccc tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tcatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccgta aacaggtaca actacagcag
1260
cctggggctg agctggtgaa gcctggggcc tcagtgaaga tgtcctgcaa ggcttctggc
1320
tacacattta ccagttacaa tatgcactgg gttaaggcaga cacctggtcg gggcctggaa
1380
tggattggag ctattnatcc agggaaatggt gatacttcct acaatcagaa gttcaaggc
1440
aaggccacac tgactgcaga caaatcctcc agcacagcct acatgcagct cagcagcctg
1500
acatctgaag actctgcggt ctattactgt gcaagatcga cttactacgg cggtgactgg
1560
tacttcaatg tctggggcgc agggaccacg gtcaccgtct ctgcaggcgg tggaggctct
1620
ggtgaggcg gttcaggagg cggtggatct caaatttttc tctccagtc tccagcaatc
1680
ctgtctgcat ctccagggga gaaggtcaca atgacttgca gggccagctc aagtgttaagt
1740
tacatccact gttccagca gaagccagga tcccccaca aaccctggat ttatgccaca
1800
tccaacctgg cttctggagt ccctgttcgc ttcagtggca gtgggtctgg gacctcttac
1860
tctctcacaa tcagtagagt ggaggctgaa gatgctgccaa cttattactg ccagcagtgg
1920
actagtaacc cacccacgtt cggtggtggg accaagctgg agatcaaacg atga
1974

<210> 48
<211> 657
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 48
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp

130	135	140
Ile Thr Arg Gln Asn Phe	Ser Arg Cys Leu Glu	Leu Gln Cys Gln Pro
145	150	155
Asp Ser Ser Thr Leu Pro	Pro Pro Trp Ser Pro Arg	Pro Leu Glu Ala
165	170	175
Thr Ala Pro Thr Ala Pro	Glu Pro Lys Ser Cys Asp	Lys Thr His Thr
180	185	190
Cys Pro Pro Cys Pro Ala	Pro Glu Leu Leu Gly Gly	Pro Ser Val Phe
195	200	205
Leu Phe Pro Pro Lys Pro	Lys Asp Thr Leu Met Ile	Ser Arg Thr Pro
210	215	220
Glu Val Thr Cys Val Val	Val Asp Val Ser His	Glu Asp Pro Glu Val
225	230	235
Lys Phe Asn Trp Tyr Val	Asp Gly Val Glu Val His	Asn Ala Lys Thr
245	250	255
Lys Pro Arg Glu Glu Gln	Tyr Asn Ser Thr Tyr Arg	Val Val Ser Val
260	265	270
Leu Thr Val Leu His Gln Asp	Trp Leu Asn Gly Lys	Glu Tyr Lys Cys
275	280	285
Lys Val Ser Asn Lys Ala	Leu Pro Ala Pro Ile	Glu Lys Thr Ile Ser
290	295	300
Lys Ala Lys Gly Gln Pro	Arg Glu Pro Gln Val	Tyr Thr Leu Pro Pro
305	310	315
Ser Arg Asp Glu Leu Thr	Lys Asn Gln Val Ser	Leu Thr Cys Leu Val
325	330	335
Lys Gly Phe Tyr Pro Ser Asp	Ile Ala Val Glu Trp Glu	Ser Asn Gly
340	345	350
Gln Pro Glu Asn Asn Tyr	Lys Thr Thr Pro Pro Val	Leu Asp Ser Asp
355	360	365
Gly Ser Phe Phe Leu Tyr	Ser Lys Leu Thr Val	Asp Lys Ser Arg Trp
370	375	380
Gln Gln Gly Asn Val Phe	Ser Cys Ser Val Met His	Glu Ala Leu His
385	390	395
Asn His Tyr Thr Gln Lys	Ser Leu Ser Leu Ser Pro	Gly Lys Gln Val
405	410	415
Gln Leu Gln Gln Pro Gly	Ala Glu Leu Val Lys	Pro Gly Ala Ser Val
420	425	430
Lys Met Ser Cys Lys Ala	Ser Gly Tyr Thr Phe	Thr Ser Tyr Asn Met
435	440	445
His Trp Val Lys Gln Thr	Pro Gly Arg Gly	Leu Glu Trp Ile Gly Ala
450	455	460
Ile Tyr Pro Gly Asn Gly	Asp Thr Ser Tyr Asn	Gln Lys Phe Lys Gly
465	470	475
Lys Ala Thr Leu Thr Ala	Asp Lys Ser Ser	Ser Thr Ala Tyr Met Gln
485	490	495
Leu Ser Ser Leu Thr Ser	Glu Asp Ser Ala	Val Tyr Tyr Cys Ala Arg
500	505	510
Ser Thr Tyr Tyr Gly Gly	Asp Trp Tyr Phe Asn	Val Trp Gly Ala Gly
515	520	525
Thr Thr Val Thr Val Ser	Ala Gly Gly Gly	Ser Gly Gly Gly Gly
530	535	540
Ser Gly Gly Gly Ser Gln	Ile Val Leu Ser Gln	Ser Pro Ala Ile
545	550	555
Leu Ser Ala Ser Pro Gly	Glu Lys Val Thr	Met Thr Cys Arg Ala Ser
565	570	575
Ser Ser Val Ser Tyr Ile	His Trp Phe Gln	Gln Lys Pro Gly Ser Ser
580	585	590

Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 595 600 605
 Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 610 615 620
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 625 630 635 640
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 645 650 655
 Arg

<210> 49
 <211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 49
 atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc
 60
 agaggagagg ttcagcttgtt ggagtctggc ggtggcctgg tgcagccagg gggctcactc
 120
 cgtttgcct gtgcagcttc tggcttcaac attaaagaca cctatataaca ctgggtgcgt
 180
 caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttataact
 240
 agatatgccg atagcgtcaa gggcggttc actataagcg cagacacatc caaaaacaca
 300
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
 360
 tggggagggg acggcttcta tgctatggac tactgggtc aaggaaccct ggtcaccgtc
 420
 tcctcg
 426

<210> 50
 <211> 142
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 50
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 20 25 30
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 35 40 45
 Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
 50 55 60
 Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
 65 70 75 80

Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
85 90 95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
115 120 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 51
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51
atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc
60
agaggagaca tccagatgac ccagtccccg agctccctgt ccgcctctgt gggcgatagg
120
gttaccatca cctgccgtgc cagtcaggat gtgaataactg ctgttagcctg gtatcaacag
180
aaaccagggaa aagctccgaa actactgatt tactcggcat ctttcctcta ctctggagtc
240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg
300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc
360
ggacagggtta ccaaggtgga gatcaaacgt
390

<210> 52
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln

	100		105		110										
His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile
				115			120					125			
Lys	Arg														

<210> 53
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53
atggatttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc
60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgccagccagg gggctcactc
120
cgtttgcct gtgcagcttc tggcttcaac attaaagaca cctatataaca ctgggtgcgt
180
caggccccgg gtaaggccct ggaatgggtt gcaaggattt atcctacgaa tggttataact
240
agatatgccg atagcgtcaa gggccgttcc actataagcg cagacacatc caaaaacaca
300
gcctacactgc agatgaacacg cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc
420
tcctcggtcta gcaccaaggg cccatcggtc ttccccctgg caccctccctc caagagcacc
480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttggaa actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagagggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcattc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggaa gagggcttcc tggcttttc
900
ccaggctctg ggcaggcaca ggcttaggtgc ccctaaccca ggcctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcggaa caccttctct cctccagat
1080
tccagtaact ccaaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg
1200

cccttagtgc gcttcatcc agggacaggc cccagccggg tgctgacacg tccaccctcca
1260
tctttccctc agcacctgaa ctccctgggg gaccgtca gtttccctttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccgaccc ctgaggtcac atgcgtggg gtggacgtga
1380
gccacgaaga ccctgaggc aagttcaact ggtacgtgg a cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggc tgcgtccctca
1500
ccgtccctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggtgc
1620
gagggccaca tggacagagg ccggctcgcc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacacctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc
1740
ggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gacacatcg cgtggagtgg gagagcaatg ggcagccgg aacaaactac aagaccacgc
1860
ctccctgtct ggactccgac ggctcccttct tcctctacag caagctcacc gtggacaaga
1920
gcagggtggca gcagggaaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a
2021

<210> 54

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

1	5						10						15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly													
	20						25						30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly													
	35						40						45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly													
	50						55						60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr													
	65						70						75
													80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr													
	85						90						95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp													
	100						105						110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala													
	115						120						125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser													
	130						135						140

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 145 150 155 160
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 165 170 175
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 180 185 190
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 195 200 205
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 210 215 220
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 225 230 235 240
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285
 Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 305 310 315 320
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 340 345 350
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 370 375 380
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 450 455 460
 Ser Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> 55
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 55
 atggatttgc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
 60
 agaggagaca tccagatgac ccagtcggc agctccctgt ccgcctctgt gggcgatagg
 120

gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag
180
aaaccaggaa aagctccgaa actactgatt tactcggcat cttccctcta ctctggagtc
240
ccttctcgct tctctggctc cagatctgg acggatttca ctctgaccat cagcagtctg
300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc
360
ggacagggtta ccaagggtgga gatcaaacgt actgtggctg caccatctgt cttcatcttc
420
ccgccccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac
480
ttcttatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac
540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc
600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat
660
cagggcctga gctcgccgt cacaaagagc ttcaacaggg gagagtgtta g
711

<210> 56
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 56
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
His Tyr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115 120 125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
210						215						220			
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
225					230					235					

<210> 57
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57
atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc
60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc
120
cgtttgcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt
180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact
240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca
300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc
420
tcctcggtcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttggc actcaggcgc cctgaccagc ggcgtgcaca cttcccgac tgcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtagagggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcattc ccggctatgc agccccagtc cagggcagca aggccaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggaa gagggcttcc tggcttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggcctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccggag gaccctgccc ctgaccataag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctccagat
1080
tccagtaact cccaatcttc tctctgcaga gccccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctgcctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacccca
1260

tctcttcctc agcacctgaa ctcctgggg gaccgtcagt cttcctcttc ccccaaaaac
1320
ccaaggacac cctcatgatc tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacagaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatcccc
1740
ggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccggtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtat gcatgaggct ctgcacaacc
1980
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2040
acagccccat ctcctccgac ttgcgtgtca aaatccgtga gctgtctgac tacctgcttc
2100
aagattaccc agtcaccgtg gcctccaacc tgcaaggacga ggagctctgc gggggcctct
2160
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2220
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2280
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2340
cctccgagca gctggtgccg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc
2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccgcccc
2460
tggaggccac agccccgaca gccccgtga
2489

<210> 58
<211> 628
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
20 25 30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly

35	40	45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly		
50	55	60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr		
65	70	75
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr		
85	90	95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp		
100	105	110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala		
115	120	125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser		
130	135	140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr		
145	150	155
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro		
165	170	175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
180	185	190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser		
195	200	205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile		
210	215	220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val		
225	230	235
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala		
245	250	255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro		
260	265	270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val		
275	280	285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp		
290	295	300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln		
305	310	315
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln		
325	330	335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala		
340	345	350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro		
355	360	365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr		
370	375	380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser		
385	390	395
		400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr		
405	410	415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr		
420	425	430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe		
435	440	445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys		
450	455	460
Ser Leu Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His		
465	470	475
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp		

485	490	495
Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp		
500	505	510
Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp		
515	520	525
Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu		
530	535	540
Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln		
545	550	555
Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu		
565	570	575
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr		
580	585	590
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser		
595	600	605
Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala		
610	615	620
Pro Thr Ala Pro		
625		

<210> 59
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59
atggatttcc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc
60
agaggagagg ttcaagctggt ggagtctggc ggtggcctgg tgcaagccagg gggctcactc
120
cgtttgcct gtgcagcttc tggcttcaac attaaagaca cctatataaca ctgggtgcgt
180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttataact
240
agatatgccg atagcgtcaa gggccgttcc actataagcg cagcacatc caaaaacaca
300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactgggtc aaggaaccct ggtcaccgtc
420
tcctcggtca gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca cttcccccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagagggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780

tggacgcata cccgctatgc agccccagtc cagggcagca aggcaaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcagggaa gagggtcttc tggcttttc
900
ccaggctctg ggcaggcaca ggcttaggtgc ccctaaccctt ggcctgcac acaaaggccc
960
agggtctggg ctcagacactg ccaagagcca tatccggag gaccctgccc ctgacctaag
1020
cccacccaa aggccaaact ctccactccc tcagctcgga caccttctct cctccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaattct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctgcgcctcc agctcaaggc gggacaggtg
1200
cccttagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctgggg gaccgtcaagt cttcctcttc ccccaaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta cggggtggtc tgcgtcctca
1500
ccgtccctgca ccaggactgg ctgaatggca aggagtacaa gtcaaggc tccaacaaag
1560
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1620
gagggccaca tggacagagg cgggctcgcc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacccctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc
1740
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1800
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1860
ctccctgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcagggaaac gtcttctcat gctccgtat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtggaggc tctggtgag
2040
gcgggttcagg aggccgtgga tctacccagg actgctcctt ccaacacagc cccatctcct
2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca
2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggcctgg
2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg
2280
agcgcgtgaa cacggagata cacttgtca ccaaattgtgc ctttcagccc ccccccagct
2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg
2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc
2460

agcccgactc ctcAACCCCTG ccACCCCCat ggAGTCCCCg gCCCTGGAG gCCACAGCCC
 2520
 cgacagcccc gtga
 2534

<210> 60
 <211> 643
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 60
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 20 25 30
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 35 40 45
 Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
 50 55 60
 Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
 65 70 75 80
 Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
 85 90 95
 Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 100 105 110
 Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
 115 120 125
 Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 130 135 140
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 145 150 155 160
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 165 170 175
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 180 185 190
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 195 200 205
 Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 210 215 220
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 225 230 235 240
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285
 Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 305 310 315 320
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

340	345	350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro		
355	360	365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr		
370	375	380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser		
385	390	395
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr		
405	410	415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr		
420	425	430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe		
435	440	445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys		
450	455	460
Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly		
465	470	475
Gly Ser Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser		
485	490	495
Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr		
500	505	510
Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu		
515	520	525
Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met		
530	535	540
Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu		
545	550	555
Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro		
565	570	575
Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu		
580	585	590
Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg		
595	600	605
Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser		
610	615	620
Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro		
625	630	635
Thr Ala Pro		

<210> 61
 <211> 1998
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 61
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 agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
 120
 ttgcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
 180

gcctccaacc tgcaggacga ggagctctgc gggggcctct ggccgctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
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360
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420
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1140
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1200
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1260
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1320
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1380
tgggttgcaa ggatttatcc tacgaatggt tatacttagat atgccgatag cgtcaaggc
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1620
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1680
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1800
ccgaaactac tgatttactc ggcattccttc ctctactctg gagtcccttc tcgcttctct
1860

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ggctccagat ctgggacgga tttcaacttg accatcagca gtctgcagcc ggaagacttc
1920
gcaacttatt actgtcagca acattatact actcctccca cgttcggaca gggtaccaag
1980
gtggagatca aacgttga
1998

<210> 62
<211> 665
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180 185 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195 200 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
210 215 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225 230 235 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
245 250 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
260 265 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
275 280 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
290 295 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305 310 315 320

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Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 325 330 335
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 340 345 350
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 355 360 365
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 370 375 380
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 385 390 395 400
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val
 405 410 415
 Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 420 425 430
 Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile
 435 440 445
 His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
 450 455 460
 Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly
 465 470 475 480
 Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln
 485 490 495
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg
 500 505 510
 Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 515 520 525
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Gly Gly
 530 535 540
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln
 545 550 555 560
 Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 565 570 575
 Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp
 580 585 590
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala
 595 600 605
 Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser
 610 615 620
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 625 630 635 640
 Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly
 645 650 655
 Gln Gly Thr Lys Val Glu Ile Lys Arg
 660 665

<210> 63
 <211> 1098

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 63

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 120
 ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
 180
 gcctccaacc tgcaaggacga ggagctctgc gggggcctct ggccgttgt cctggcacag
 240
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 360
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 480
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 600
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 720
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 900
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 960
 cctgacccta tattgttgat gaaaagtgtc agaaatagtt gttggctaa agatgcagaa
 1020
 tatggactct attccatcta tcaaggggaa atatttgagc ttaaggaaaa tgacagaatt
 1080
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 1098
 gccttttag ttggctaa

<210> 64

<211> 365

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu
1									10				15		
Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe
									25				30		
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
									35			45			
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
									50			55	60		
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
									65			70	75		80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly

85	90	95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala		
100	105	110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser		
115	120	125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp		
130	135	140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro		
145	150	155
Asp Ser Ser Thr Leu Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala		
165	170	175
Thr Ala Pro Thr Ala Pro Gly Gly Ser Gly Gly Gly Ser		
180	185	190
Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala		
195	200	205
His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn		
210	215	220
Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser		
225	230	235
Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly		
245	250	255
Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr		
260	265	270
Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys		
275	280	285
Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile		
290	295	300
Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu		
305	310	315
Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu		
325	330	335
Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met		
340	345	350
Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly		
355	360	365

<210> 65
 <211> 1203
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 65
 atgacagtgc tggcgccagc ctggagccca acaacctatac tcctcctgtct gctgctgctg
 60
 agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
 120
 ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
 180
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
 240
 cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
 300

gtgaacacgg agatacacatt tgtcaccaaa tgtgccttc agccccccc cagctgtctt
 360
 cgcttcgtcc agaccaacat ctcccgccctc ctgcaggaga cctccgagca gctggtggcg
 420
 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
 480
 gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca
 540
 gccccgatga agcagatcga ggacaaaatt gaggaaatcc tgtccaagat ttaccacatc
 600
 gagaacgaga tcgcccggat taagaaactc attggcgaga cctctgagga aaccatttct
 660
 acagttcaag aaaagcaaca aaatatttct cccctagtga gagaaagagg tcctcagaga
 720
 gtgcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc
 780
 aagaatgaaa aggctctggg ccgcaaaata aactcctggg aatcatcaag gagtggcat
 840
 tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcattccatga aaaagggttt
 900
 tactacatct attcccaaac atactttcga tttcaggagg aaataaaaga aaacacaaag
 960
 aacgacaaac aaatggtcca atatatttac aaatacaca aaatacaca gttatcctga ccctatattg
 1020
 ttgatgaaaa gtgcttagaaa tagttgtgg tctaaagatg cagaatatgg actctattcc
 1080
 atctatcaag gggaatatt tgagcttaag gaaaatgaca gaattttgt ttctgtaca
 1140
 aatgagcact tgatagacat ggaccatgaa gccagtttt ttggggcctt ttttagttggc
 1200
 taa
 1203

<210> 66
 <211> 400
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66
 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser

115	120	125
Arg Leu Leu Gln Glu Thr Ser	Glu Gln Leu Val Ala	Leu Lys Pro Trp
130	135	140
Ile Thr Arg Gln Asn Phe Ser Arg Cys	Leu Glu Leu Gln Cys Gln	Pro
145	150	155
Asp Ser Ser Thr Leu Pro Pro Trp	Ser Pro Arg Pro Leu Glu	Ala
165	170	175
Thr Ala Pro Thr Ala Pro Met Lys	Gln Ile Glu Asp Lys	Ile Glu Glu
180	185	190
Ile Leu Ser Lys Ile Tyr His	Ile Glu Asn Glu	Ile Arg Ile Lys
195	200	205
Lys Leu Ile Gly Glu Thr Ser	Glu Glu Thr Ile Ser	Thr Val Gln Glu
210	215	220
Lys Gln Gln Asn Ile Ser Pro	Leu Val Arg Glu Arg	Gly Pro Gln Arg
225	230	235
Val Ala Ala His Ile Thr Gly	Thr Arg Gly Arg	Ser Asn Thr Leu Ser
245	250	255
Ser Pro Asn Ser Lys Asn Glu	Lys Ala Leu Gly Arg	Lys Ile Asn Ser
260	265	270
Trp Glu Ser Ser Arg Ser Gly	His Ser Phe Leu Ser	Asn Leu His Leu
275	280	285
Arg Asn Gly Glu Leu Val Ile His	Glu Lys Gly Phe	Tyr Tyr Ile Tyr
290	295	300
Ser Gln Thr Tyr Phe Arg	Phe Gln Glu Glu	Ile Lys Glu Asn Thr Lys
305	310	315
Asn Asp Lys Gln Met Val Gln	Tyr Ile Tyr Lys	Tyr Thr Ser Tyr Pro
325	330	335
Asp Pro Ile Leu Leu Met Lys	Ser Ala Arg Asn Ser	Cys Trp Ser Lys
340	345	350
Asp Ala Glu Tyr Gly Leu Tyr	Ser Ile Tyr Gln Gly	Gly Ile Phe Glu
355	360	365
Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val	Thr Asn Glu His Leu	
370	375	380
Ile Asp Met Asp His Glu Ala Ser Phe	Phe Gly Ala Phe Leu Val	Gly
385	390	395
		400

<210> 67
 <211> 1749
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 67
 atgacagtgc tggcgccagc ctggagccca acaaacctatc tcctcctgct gctgctgctg
 60
 agctcgggac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac
 120
 ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
 180
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggccggcttgt cctggcacag
 240
 cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
 300

gtgaacacgg agatacac tt tgtcaccaaa tgtgccttc agccccccc cagctgtctt
360
cgttcgtcc agaccaacat ctcccgcc tcgaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca
540
gccccggagc ccaaattctg tgacaaaact cacacatgcc caccgtgcc agcacctgaa
600
ctcctgggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtcaaggc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca
960
tcccggatg agctgaccaa gaaccaggc agcctgacct gcctggtcaa aggcttcttat
1020
cccagcgaca tcgccgtgga gtggagagc aatggcagc cggagaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctt acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tcatgtcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctccggta aagttagaga aagaggtcct
1260
cagagatg cagtcacat aactggacc agaggaagaa gcaacacatt gtcttctcca
1320
aactccaaga atgaaaaggc tctggccgc aaaataaaact cctggaaatc atcaaggagt
1380
gggcattcat tcctgagcaa cttgcacttg aggaatggtg aactggtcat ccatgaaaaa
1440
gggtttact acatctattc ccaaacatac ttgcatttc aggaggaaat aaaagaaaaac
1500
acaagaacg acaaacaat ggtccatat atttacaaat acacaagtta tcctgaccct
1560
atattgtga tgaaaagtgc tagaaatagt tggtggtcta aagatgcaga atatggactc
1620
tattccatct atcaaggggg aatatttgag cttaaggaaa atgacagaat ttttgttct
1680
gtaacaaatg agcacttgat agacatggac catgaagcca gttttttgg ggcctttta
1740
gttggctaa
1749

<210> 68
<211> 582
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 68

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180 185 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195 200 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
210 215 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225 230 235 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
245 250 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
260 265 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
275 280 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
290 295 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305 310 315 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
325 330 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
340 345 350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
355 360 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
370 375 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385 390 395 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Arg
405 410 415
Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
420 425 430

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
435 440 445
Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
450 455 460
Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
465 470 475 480
Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
485 490 495
Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
500 505 510
Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
515 520 525
Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
530 535 540
Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
545 550 555 560
Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
565 570 575
Gly Ala Phe Leu Val Gly
580

<210> 69

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 69

gcactcgagt tttacccgga gacagggaga g

31

<210> 70

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 70

gagcccaaat cttgtgacaa aac

23